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FETAL HEALTH RISK STATUS IDENTIFICATION SYSTEM BASED ON CARDIOTOCOGRAPHY DATA USING EXTREME GRADIENT BOOSTING WITH ISOLATION FOREST AS OUTLIER DETECTION

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ABSTRACT

Premature birth and birth defects contribute significantly to infant mortality, highlighting the need for early identification of fetal health risks. This study uses XGBoost for fetal health classification, integrating IForest for outlier detection to improve model performance. By varying the contamination percentage, learning rate (η), maximum depth, and n_estimator, the best results were achieved at CP = 8%, η = 0.01, max_depth = 7, and n_estimator = 100, which resulted in 100% accuracy, sensitivity, and specificity with a calculation time of 0.36 seconds. IForest effectively reduced the dataset from 2126 to 1956 samples by removing outliers, improving accuracy by 3.76%, and reducing computation time by 0.51 seconds. These findings suggest that IForest improves classification efficiency while maintaining high predictive performance, supporting early identification of fetal health risks to aid timely medical intervention.

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1. INTRODUCTION

Premature birth is one of the leading causes of infant mortality in the world. According to a report from the World Health Organization (WHO), in 2019, around 900,000 children died from complications associated with premature birth. The number of babies born prematurely is also increasing, estimated to reach 13.4 million cases in 2020. Most of these cases are triggered by infections or complications during pregnancy [1]. In addition to the risk of infant mortality, preterm birth can also increase the likelihood of long-term health problems, including birth defects. The contribution of birth defects globally as a cause of death of children under 5 years of age continues to increase. Between 2000 and 2021, in the Southeast Asia Region, including Indonesia, it increased from 4% to 11%, equivalent to the death of 300 children under the age of 5 every day [2]. Factors that cause birth defects include genetics, exposure to pollutants, lifestyle choices, and socioeconomic conditions with low and middle-income [3].

Based on the high mortality rate, early detection is needed to identify health problems early on, one of which is by monitoring the fetal heart rate, which can indicate its health condition [4]. The heart rate that is monitored by the doctor can evaluate the overall condition of the fetus with the Cardiotocography (CTG) tool. CTG is superior to other fetal examination tools because it monitors the fetal heart rate and uterine contractions continuously and in real-time for 15-20 minutes [5]. CTG provides more comprehensive data on fetal well-being than ultrasound, which only provides visual images, or a Doppler fetal monitor, which monitors heart rate irregularities. In addition, CTG is more objective with quantitative data than subjective palpation of contractions, and more relevant than laboratory tests that do not directly monitor fetal condition during labor [6].

Efforts to efficiently identify fetal health risks through CTG can be made by applying Machine Learning (ML). ML is implemented to automate and improve the accuracy of the risk identification process compared to manual methods because it relies heavily on the subjective expertise of obstetricians and is prone to human error [7]. Various ML algorithms have been applied for fetal health classification, using Naive Bayes (NB), J48, Random Forest (RF), Logistic Regression (LR), K-Nearest Neighbors (KNN), Support Vector Machines (SVM), and Neural Network Multi-Layer Perceptron (NNMLP) methods. The accuracy obtained from these methods varies with a difference of more than 13%; the highest accuracy is obtained with RF of 93.41% [8]. On the other side, there are studies that use the RF method which is superior with an accuracy of 98% compared to Decision Tree (DT), KNN, Voting Classifier, SVM, and LR which have an accuracy of 96%, 90%, 97%, 97%, and 96% respectively [9]. Based on previous research on fetal health classification systems, the best accuracy value is obtained in the RF method.

Previous research shows that the Random Forest (RF) method produces the best accuracy in fetal health classification. However, this method has a weakness, namely, the resulting trees are independent and do not utilize prediction errors in the previous tree to be improved iteratively, as is done by the boosting method [10]. The Extreme Gradient Boosting (XGBoost) method can overcome these shortcomings by iteratively updating the model to improve predictions [11]. The superiority of XGBoost was proven in diabetes classification research, which achieved the highest accuracy of 82.68% compared to KNN, DT, RF, NB, SVM, and NNMLP methods [12]. In addition, pneumonia severity classification research showed XGBoost had an accuracy of 93%, outperforming the LR and RF methods [13]. In a study of pregnant women's health classification, XGBoost also obtained the best accuracy of 90%, compared to other methods such as Adaptive Boosting (AdaBoost) and Gradient Boosting Trees (GBT) [14].

Although previous studies have shown the efficiency and superiority of the XGBoost method in classification, each dataset has different characteristics or high variation and uneven distribution, so special handling is needed to detect outlier data because it can affect the results of analysis and classification models [15]. One of the outlier detection methods is Isolation Forest (IForest), which separates anomalous data using binary trees [16]. IForest is proven to be superior to One-Class SVM (OCSVM) with 90 seconds faster computation time [17]. IForest is also superior in detecting outlier data, as evidenced by an accuracy value of 99.72% compared to Local Outlier Factor (LOF) with an accuracy of 99.62% [18]. IForest can improve model accuracy by 1%-5% compared to without IForest [19].

Based on the background that has been presented with the support of previous research as a reference, it has proven that the XGBoost method is superior for classification, with IForest as an outlier detection method that is more efficient than other outlier detection methods. The purpose of this research is to create a fetal health risk status identification system with high-accuracy results based on IForest as an outlier data detection method and the classification method, namely, XGBoost with parameter tuning. The results of this

fetal health classification are expected to contribute to and assist medical personnel in taking wise action before it gets worse.

2. RESEARCH METHODS

The data in this research is secondary data sourced from the Kaggle website [20]. The data consists of 2126 total data points with 1655 data points classified as normal, 295 data points classified as suspect, and 176 data points classified as pathological, so there is an imbalance in the dataset. This data has 21 factor variables and 1 fetal health status variable. Data balancing was not performed because this is sensitive medical data, where errors in the generation of synthetic data could risk changing the original characteristics of the data and affect the accuracy of the classification results. Table 1 is a sample of research data where the factor variables are numeric and categorical data types. This data includes various variables that describe fetal health conditions. The factor variables are Baseline (x_1), Accelerations (x_2), Fetal Movement (x_3), Uterine Contractions (x_4), Light Decelerations (x_5), Severe Decelerations (x_6), Prolonged Decelerations (x_7), Abnormal Short-Term Variability (x_8), Mean Value of Short-Term Variability (x_9), Percentage of Time with Abnormal Long-Term Variability (x_{10}), Mean Value of Long-Term Variability (x_{11}), Histogram Width (x_{12}), Histogram Min (x_{13}), Histogram Max (x_{14}), Histogram Number of Peaks (x_{15}), Histogram Number of Zeros (x_{16}), Histogram Mode (x_{17}), Histogram Mean (x_{18}), Histogram Median (x_{19}), Histogram Variance (x_{20}), and Histogram Tendency (x_{21}) with values of (-1) or left asymmetric, (0) or symmetric, and 1 or right asymmetric. The target variable has three classes, namely normal, suspect, and pathologic, which describe the health status of the fetus [11].

Table 1. Sample of Research Data

x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8	x_9	⋯	x_{21}	Target
120	0	0	0.0	0.0	0.0	0.0	73.0	0.5	⋯	1	Suspect
132	0.006	0	0.006	0.003	0.0	0.0	17.0	2.1	⋯	0	Normal
133	0.003	0	0.008	0.003	0.0	0.0	16.0	2.1	⋯	0	Normal
134	0.003	0	0.008	0.003	0.0	0.0	16.0	2.4	⋯	1	Normal
132	0.007	0	0.008	0.0	0.0	0.0	16.0	2.4	⋯	1	Normal
134	0.001	0	0.01	0.009	0.0	0.002	26.0	5.9	⋯	0	Pathologic
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋱	⋮	⋮
142	0.002	0.002	0.008	0.0	0.0	0.0	74.0	0.4	⋯	0	Normal

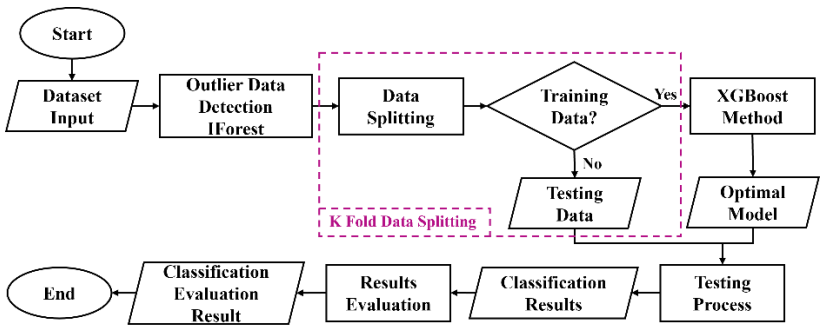

Figure 1. Flowchart of Research

Figure 1 is a flowchart showing the classification process using the XGBoost method with outlier handling through IForest. The process starts with entering the dataset, which then goes through the outlier detection stage using IForest. Data detected as outliers will be removed from the dataset. After the data is cleaned, it is then divided into training and testing data using K-Fold Cross Validation. If the data is training data, the XGBoost method is used to build an optimal classification model, and testing data will be used to test the performance of the model. The test results produce a classification, which is then evaluated to assess the accuracy, sensitivity, and specificity of the model's performance using the confusion matrix.

2.1 Cardiotography (CTG)

Cardiotocography (CTG) is an ultrasonic monitoring technology specifically designed to facilitate medical experts in examining fetal heart rate (FHR) variations and uterine contractions (UC) [21]. This examination can prevent adverse consequences, such as death in the first week of life (perinatal), and hypoxic brain injury, which is a major cause of disability in the future [22]. CTG examination is usually performed in the third trimester of pregnancy or during labor to ensure fetal health [23]. The output of CTG examination is a graph or recording that shows two main parameters, namely the fetal heart rate on the upper graph where the yellow color indicates FHR worth 150 - 180 beats per minute (bpm) and the pink indicates FHR worth above 180 - 250 bpm, while the lower graph is uterine contractions as in Figure 2 [24].

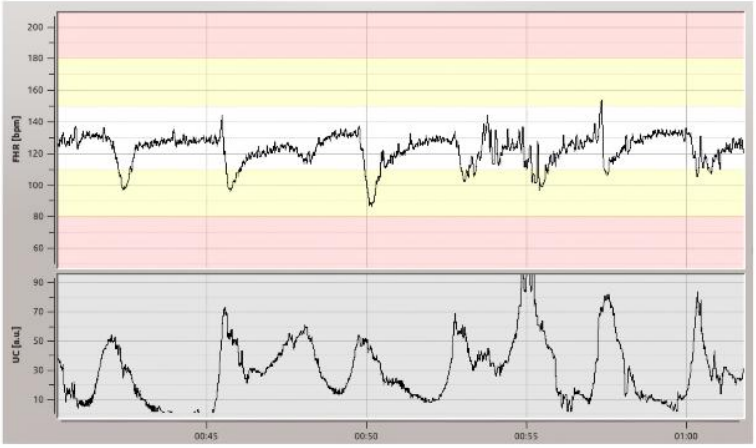

Figure 2. CTG Tool Output Result Graph

Some indicators in the examination using CTG are baseline, accelerations, decelerations, fetal movement, uterine contractions, variability, and histograms on the frequency distribution of fetal heart rate [7]. The output of CTG, as shown in Figure 2, is in the form of a graph, which visually presents the pattern of fetal heart rate and uterine contractions. However, the interpretation of these graphs can be subjective and susceptible to differences in judgment between users. Therefore, there is an automated analysis tool of CTG recordings, SisPorto 2.0 [25]. This tool was created to provide users with measurable and consistent reports, with a processing time of about 10 minutes. The computerized system also allows evaluation of parameters that the human eye cannot reliably assess [26]. Baseline is the fetal baseline heart rate measured over 10 minutes. The normal range of baseline is 110-160 beats per minute (bpm), while baseline FHR Tachycardia > 160 bpm for ≥ 10 minutes and baseline FHR Bradycardia < 110 bpm for ≥ 10 minutes. These values reflect the resting fetal heart rate without significant accelerations or decelerations. Fetal movement refers to fetal movements that may affect the fetal heart rate. These movements are usually recorded as accelerations on CTG and indicate that the fetus is active and healthy [27].

Uterine contractions can detect a decrease in fetal heart rate followed by a rapid increase. Therefore, electronic monitoring of fetal heart rate by CTG should be started immediately to avoid adverse outcomes in the pre-born baby [28]. Variability is the variation in the time interval between each fetal heartbeat. Good variability indicates a healthy fetal nervous system and the ability of the fetus to adapt to changes. A histogram is a graphical representation of the frequency distribution of fetal heart rate over some time [7]. Histograms assist in visualizing how the fetal heart rate varies during measurements and can provide additional information about fetal well-being [24].

The classification of fetal health is divided into 3, namely normal, suspect, and pathologic, according to the International Federation of Gynecology and Obstetrics (FIGO). FIGO is a global organization that focuses on improving women's reproductive health through education and policy development. FIGO provides guidelines and clinical practice standards for clinicians in the field of gynecology and obstetrics [29]. The normal grade indicates a stable and responsive fetal heart rate pattern, indicating a healthy fetal condition. The suspect class reflects some abnormality, such as decreased variation or delay, which requires further monitoring to ensure fetal well-being. Pathologic class indicates signs of significant fetal distress, requiring immediate medical intervention, such as delivery, to protect fetal health [8].

2.2 Isolation Forest (IForest)

Isolation Forest (IForest) is a method used to detect outliers or anomalies. The IForest method is ensemble-based by applying unsupervised learning [30]. This method focuses on isolating anomalies directly based on the principle that they are rare and highly distinct, making them easier to isolate than normal points. IForest forms a collection of isolation trees with each isolation tree (iTree) working not by classifying but by isolating data points. An important element in this method is path length, which is the number of edges a data point crosses in the tree before it is isolated. A shorter path length indicates a higher likelihood that the point is an anomaly, as it is easier to isolate. The IForest calculation step begins by calculating the amount of Contamination Percentage (CP), which is the approximate proportion of data that are outliers in the dataset. This parameter is important because it helps the method to adjust its sensitivity in detecting anomalies with the formula in **Equation (1) [31]**.

$$An = b \times d \tag{1}$$

where An is the number of outlier data points with contamination percentage b, and d is the number of data points in a variable.

Build an isolation tree (iTree) by randomly selecting features, which are then divided by a random value between the minimum and maximum values of the variable, and calculate the anomaly score $S(x,n)$ for each data.

$$E\big(h(x)\big) = \frac{\sum_{i=1}^{t} h(x,i)}{t} \tag{2}$$

$$H(n) = \ln(n) + 0.57772156649 \tag{3}$$

$$c(n) = \begin{cases} 2H(n-1) - \dfrac{2(n-1)}{n} & ;\ n > 2 \\ 1 & ;\ n = 2 \\ 0 & ;\ n < 2 \end{cases} \tag{4}$$

$$S(x,n) = 2^{-\frac{E(h(x))}{c(n)}} \tag{5}$$

where $\sum_{i=1}^{t} h(x,i)$ is the number of path lengths at point x and t is the number of trees formed. $E\big(h(x)\big)$ is the expectation or average of $h(x,i)$ with $H(n)$ being a harmonic function, and $S(x,n)$ is the anomaly score of the data x for n data points. The anomaly scores are sorted from highest to lowest to select a number of data points that are considered anomalies based on An number of data points from the largest score. The final result is the value of $S(x,n)$ is -1 if the data is classified as an anomaly and 1 if the data is classified as not an anomaly.

2.3 Extreme Gradient Boosting (XGBoost)

Extreme Gradient Boosting (XGBoost) is a method that evolved from Random Forest (RF). RF is a Bootstrap Aggregating (bagging) method that builds a number of decision trees (trees) from sample data independently. This process uses the concept of bagging with data replacement (replacement) and random variable selection for each tree, so that the final decision is taken based on the most votes [32]. Bagging has the disadvantage that each model is built independently. This makes it less effective in correcting errors that often occur in previous models. These shortcomings can be complemented by boosting, which builds models gradually, where each new model will learn the mistakes made by the previous model, so boosting is more effective in improving accuracy by reducing bias and improving classification performance [33].

The method that adopts the concept of boosting is Extreme Gradient Boosting (XGBoost). The basic concept of the XGBoost method is iterative learning to reduce the loss function [34]. The decision tree in this method applies an ensemble technique where the model will be continuously updated to correct errors in the previous model [32]. XGBoost is designed to maximize speed and efficiency through techniques such as tree pruning. This method also creates decision trees sequentially, so it has strong sequential capabilities [35].

In **Figure 3** below is a visualization of the decision tree in the XGBoost method, which begins with instances, which are input data or samples that will be predicted by the model. Each instance will go through a series of processes in the XGBoost model. Instances produce as many as t trees (Tree-1, Tree-2, to Tree-t)

where each tree processes and produces outputs $(f_1(x_i), f_2(x_i),$ to $f_t(x_i))$. Each tree also considers the residuals from the previous tree to improve its classification performance. The results of each tree are summed up to obtain the final result. This iterative process allows XGBoost to create a strong predictive model by combining the outputs of multiple weak models [36].

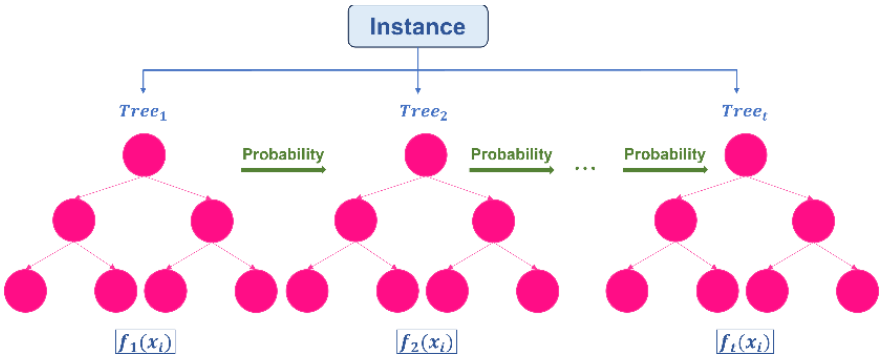

Figure 3. Architecture in XGBoost

Based on Figure 3, the classification result value at step t is symbolized $\hat{y}_i^{(t)}$ with $f_m(x_i)$ indicating the t-th tree model of the dataset x_i as in Equation (6) below.

$$\hat{y}_i^{(t)} = \sum_{m=1}^{t} f_m(x_i) \tag{6}$$

The steps in implementing XGBoost are initializing the number of trees (estimator), tree depth (max depth), gamma (γ), learning rate (η), lambda (λ), and initial probability (P) which are then calculated with the softmax function, as for the formula in Equation (7) [37].

$$s(P_i) = \frac{e^{(P)}}{\sum_{i=1}^{nc} e^{(P)}} \tag{7}$$

where nc is the number of classes.

The next step is to calculate the residual (gradient) value (e) by subtracting the initial probability value from the target of each class, which is worth 1 in the calculated class. The calculation formula is like Equation (8) [37].

$$e_i = P_i - y_i \tag{8}$$

$$h = \left(2P_i \times (1 - P_i)\right) \tag{9}$$

$$SS = \frac{\left(\sum_{i=1}^{n} e_i\right)^2}{\left(\sum_{i=1}^{n} (2P_i \times (1 - P_i)) + \lambda\right)} \tag{10}$$

$$Gain = \left(SS_{left} + SS_{right}\right) - SS_{root} \tag{11}$$

$$w = -\frac{\left(\sum_{i=1}^{n} e_i\right)}{\left(\left(\sum_{i=1}^{n} h\right) + \lambda\right) \times \eta} \tag{12}$$

$$Co_i = \sum_{i=1}^{n} (2P_i \times (1 - P_i)) \tag{13}$$

In this context, h is the Hessian; SS is the Similarity Score, with Pi is the probability for the i-th observation up to n data points, with λ as the regulation parameter. Gain is used to determine the performance of residual grouping, similar to the separation into two groups; the highest Gain value will be selected as the branch that separates the residuals [38]. w is the value of the leaf or output on the branch that has reached max depth, with Co_i is the minimum number of residuals in each leaf.

In XGBoost, pruning of the tree is performed by calculating the difference between the Gain on the lowest branch or a branch of the tree with a predetermined γ (gamma) value. If the difference obtained is positive, then no pruning will be done on the branch. However, if it is negative, then pruning is done, so the calculation continues on the positive branch [39]. The tree pruning formula is as in Equation (14).

$$G - \gamma < 0 \tag{14}$$

The next step is to update the probability with the formula as in the following Equation (15) [38].

$$\log(odds) = \log\left(\frac{P}{1-P}\right) \tag{15}$$

$$P_i^{t+1} = \log(odds) + \left(\sum_{i=1}^{m} w \times \eta\right) \tag{16}$$

Odds are defined as the probability of success divided by the probability of failure, formulated by **Equation (15) [38]**. Whereas log(*odds*) is the logarithm of the odds formulated as in **Equation (16)**. P_i^{t+1} the probability of the $(t\ +\ 1)$ −th tree is calculated, where $\sum_{i=1}^{m} w$ is the leaf sum with m is the number of leaves formed from the tree in each class **[37]**.

$$f(x_i) = P + \sum_{i=1}^{t} w \tag{17}$$

$f(x_i)$ is the classification result calculated by combining the leaf values. In creating the next tree, the new residual value is used. This process is repeated until the residual value is very small or until the number of estimators is reached.

$$s\big(f(x_i)\big) = \frac{e^{(f(x_i))}}{\sum_{i=1}^{nc} e^{(f(x_i))}} \tag{18}$$

Returning the probability value into a multiclass classification result can use the softmax function as in **Equation (18)**. This function returns the probability for each class, and the probability of the corresponding target class will have a high value **[40]**.

2.4 Confusion Matrix (CM)

Confusion Matrix (CM) multiclass is used to measure the performance of the classification model against each class of data in more than two classes, visualized in **Table 2 [41]**. If the actual data of the focused class is predicted correctly, it is called a True Positive (TP); if incorrect, it is a False Negative (FN). If the data of another class is predicted as the focused class, it is called False Positive (FP); the prediction of another class is called True Negative (TN) **[15]**.

Table 2. Visualization of Confusion Matrix

		Prediction		
		N	**S**	**P**
Actual	**N**	TP	FN	FN
	S	FP	TN	TN
	P	FP	TN	TN

Normal (a)

		Prediction		
		N	**S**	**P**
Actual	**N**	TN	FP	TN
	S	FN	TP	FN
	P	TN	FP	TN

Suspect (b)

		Prediction		
		N	**S**	**P**
Actual	**N**	TN	TN	FP
	S	TN	TN	FP
	P	FN	FN	TP

Pathologic (c)

Accuracy is a value that indicates the accuracy of the classification system being developed, with the formula in **Equation 19 [42]**.

$$\text{Accuracy} = \frac{\sum_{i=1}^{nc} TP_i}{nx} \times 100\% \tag{19}$$

where TP_i is the sum of TP per focused class with TP_1 being the TP in class N (normal), nc is the number of classes, and nx is the number of input data.

High sensitivity indicates the effectiveness of the classification system in identifying potentially pathologic fetal health risks, as shown in **Equation (20) [43]**.

$$\text{Sensitivity} = \frac{\sum_{i=1}^{nc} \frac{TP_i}{TP_i + FN_i}}{nc} \times 100\% \tag{20}$$

A high specificity indicates the effectiveness of the classification system in identifying fetuses with normal health conditions, as shown in **Equation (21) [44]**.

$$\text{Spesificity} = \frac{\sum_{i=1}^{nc} \frac{TN_i}{TN_i + FP_i}}{nc} \times 100\% \tag{21}$$

3. RESULTS AND DISCUSSION

3.1 Parameter Tuning Experiment Scheme

Parameter tuning in the XGBoost model aims to improve performance by adjusting various parameters that affect the learning process of the model. The selection of parameter values in this study is based on references from journals that use the same or similar methods and data characteristics, so it is expected to produce an optimal configuration. In general, the journal references show that the tested parameter combinations have given good results in previous studies. The tested parameters include learning rate (η) with values of 0.001 and 0.01 [45], max depth of 3, 5, and 7 [46], and estimators of 50 and 100 [47]. A lower η slows convergence but enhances model stability, while a higher η speeds up learning but risks overshooting optimal solutions. Increasing max depth allows the model to capture complex patterns but raises overfitting risks and computational costs. A higher number of estimators improves performance but increases training time. These parameters were systematically tested to find the optimal configuration for balancing accuracy, generalization, and efficiency.

3.2 Outlier Detection Using Isolation Forest (IForest)

In this research, outlier detection is performed using Isolation Forest (IForest) with a contamination percentage (CP) of 8% and the number of trees (iTree) of 100, which is the default value of IForest. The 8% CP selection is based on trials with a range of 5%-10%, where the 8% CP produces the highest classification accuracy, so it is used in the next process. Outlier detection is performed before the division of training and testing data to keep the data distribution representative. The detected outliers are removed, while the inlier data is retained and used in the classification process.

After outlier handling, the mean value of the inlier data remains in line with the original data, indicating that the central tendency has not changed much. However, the standard deviation is lower, indicating a decrease in variability due to outlier removal. The maximum values of many variables also decreased, indicating success in removing extreme values, while the minimum values remained relatively stable. In categorical variables such as Histogram Tendency, the mode value remains 0 before and after the treatment, indicating that the distribution of dominant categories has not changed. Thus, IForest is effective in stabilizing the distribution of data without changing the main characteristics, thus improving the quality of data in classification.

3.3 Classification Using the Extreme Gradient Boosting (XGBoost) Method

In this research, the XGBoost method is used for classification. After going through the pre-processing stage and before starting the classification process, the next step is to divide the data into two parts, namely training and testing. This splitting is done using the K-Fold Cross Validation method with K = 5. The test results are shown in Table 3 and Table 4.

Table 3. Results of Testing with Outlier Handling

max depth	estimator	η	Accuracy (%)	Sensitivity (%)	Specificity (%)	Time (s)
3	50	0.001	94.12	93.75	95.22	0.11
		0.01	96.16	95.66	96.71	0.12
	100	0.001	94.88	94.08	96.70	0.24
		0.01	97.19	97.35	97.94	0.22
	Average		95.59	95.21	96.64	0.18
5	50	0.001	97.70	97.95	98.39	0.19
		0.01	98.47	98.85	99.07	0.15
	100	0.001	97.70	96.59	98.77	0.24
		0.01	98.47	99.03	99.15	0.33

max depth	estimator	η	Accuracy (%)	Sensitivity (%)	Specificity (%)	Time (s)
7	Average		98.08	98.10	98.85	0.23
	50	0.001	99.23	97.56	99.62	0.93
		0.01	99.23	99.59	99.64	0.21
	100	0.001	99.23	97.56	99.62	1.12
		0.01	100	100	100	0.36
	Average		99.42	98.68	99.72	0.66

Table 3 shows the results of an experiment with outlier handling, which shows that the best average trial is at max depth 7 with accuracy, sensitivity, and specificity values of 99.42%, 98.68%, and 99.72%, respectively, which has a computation time of 0.66s indicating that the model is more stable at a max depth of 7. The best results on average are obtained at estimator 100 with η as much as 0.01. The accuracy, sensitivity, and specificity values obtained are 100% with a computation time of 0.36s. The classification results on data without outlier handling are shown in **Table 4**.

Table 4. Results of Testing Without Outlier Handling

max depth	estimator	η	Accuracy (%)	Sensitivity (%)	Specificity (%)	Time (s)
3	50	0.001	92.94	83.72	91.28	0.13
		0.01	93.65	83.85	91.54	0.13
	100	0.001	93.18	83.82	91.37	0.26
		0.01	95.06	85.66	92.68	0.22
	Average		93.71	84.26	91.72	0.18
5	50	0.001	94.82	86.34	92.90	0.20
		0.01	95.29	87.76	93.68	0.19
	100	0.001	94.82	86.34	92.90	0.37
		0.01	95.53	89.08	94.38	0.41
	Average		95.12	87.38	93.46	0.29
7	50	0.001	95.29	86.98	93.38	1.33
		0.01	95.76	89.17	94.47	0.41
	100	0.001	95.29	86.98	93.38	0.77
		0.01	96.24	90.59	95.25	0.87
	Average		95.65	88.43	94.12	0.84

Table 4 is the result of the experiment without outlier handling which shows that the best average of the experiment is at max depth 7, the accuracy, sensitivity, and specificity values obtained are 95.65%, 88.43%, and 94.12%, respectively, with a computation time of 0.84s, indicating that the model is more stable at max depth 7. The best results on average were obtained at estimator 100 with η of 0.01. The accuracy, sensitivity, and specificity values obtained were 96.24%, 90.59%, and 95.25%, respectively, which had a computation time of 0.87s. The bar graph shown in **Figure 4** is a visualization of the comparison of the classification evaluation results on data with and without outlier handling.

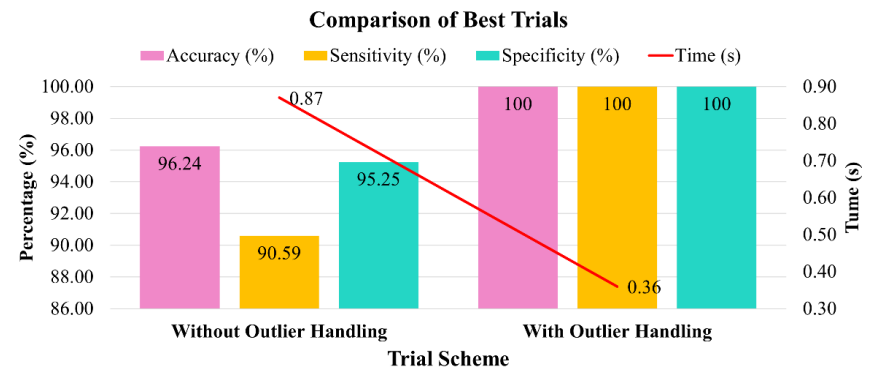

Figure 4. Comparison Chart of Experiment Results

Based on **Figure 4**, which is the visualization result of the best experiment with and without outlier handling. The left y-axis shows the accuracy, sensitivity, and specificity in %, and the right y-axis shows the computation time (s). The results show that the model with outlier handling achieved 100% accuracy, sensitivity, and specificity, while the model without outlier handling only achieved accuracy, sensitivity, and specificity of 96.24%, 90.59%, and 95.25%, respectively. This indicates that handling outliers with IForest significantly improves the performance of the model. In addition to the improvement in accuracy, sensitivity, and specificity, the model with IForest also shows a faster computation time of 0.51 seconds, compared to the model without outlier handling. This is due to the smaller amount of data after outliers are handled, thus speeding up the Gain computation process in the XGBoost method. Thus, the use of IForest not only improves the model evaluation results but also provides efficiency in terms of computation time.

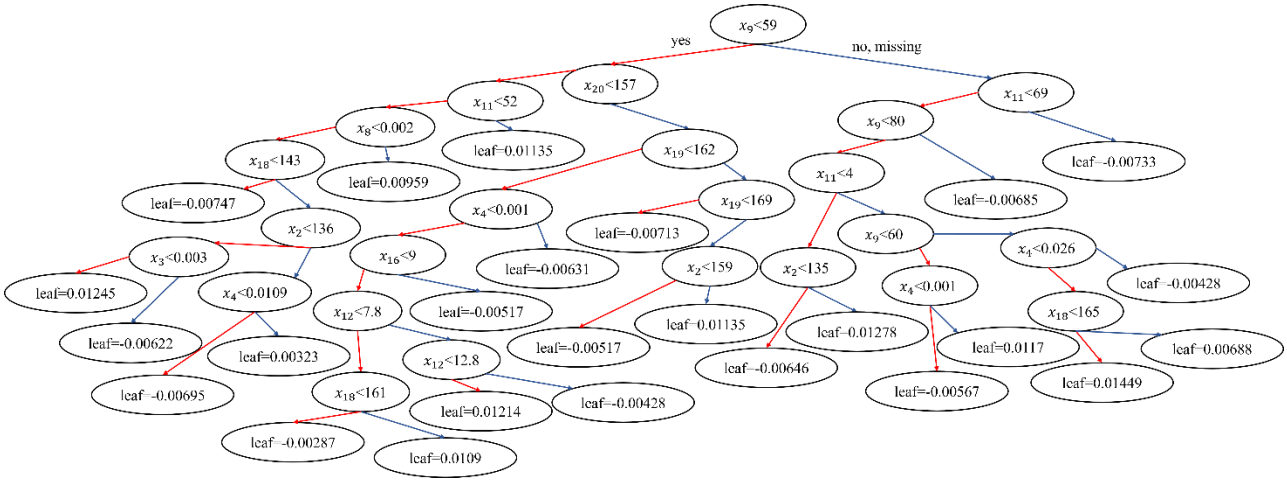

Figure 5. First Decision Tree on the Best Trial

The decision tree in **Figure 5** represents the decision-making process of the XGBoost model in predicting the data class. The flow starts from the root node, which is the first condition. If this condition is met, the model moves to the red left branch (yes). Otherwise, it moves to the blue right branch (no). This process continues at each node, where each feature x_1 to x_{21} is compared to a specific value to further split the data. At each branching, eligible data proceeds to the left branch, while those that do not proceed to the right branch. At the end of the path (leaf), there is a value that indicates the final result or prediction of the model. This value reflects the strength of the prediction on that path, where positive values indicate a trend towards one class and negative values towards another. This flow shows how the model filters the data through a series of feature-based decisions to reach the final prediction. As this is a multi-class classification, XGBoost builds one tree for each class, where each tree focuses on distinguishing one class from another.

To determine the comparative results of this study with other studies, the following is a comparison of the evaluation results of fetal health status classification systems conducted in several previous studies based on the same dataset. **Table 5** below shows the comparison, which can provide an overview of the strengths and weaknesses of the various approaches that have been tested.

Table 5. Performance Comparison on Classification of CTG Result Data

Method	Accuray (%)	Sensitivity (%)	Specificity (%)	Time (s)
DT [48]	92	91	-	-
RF [7]	95.77	95.77	-	-
Extreme Learning Machine (ELM) [49]	93.42	-	-	0.18
Categorical Boosting (CatBoost) [50]	99	99	-	-
XGBoost + IForest (our purpose)	100	100	100	0.36

Table 5 shows a comparison of the performance of several classification methods on Fetal Health data from CTG based on accuracy (%), sensitivity (%), specificity (%), and duration time (s) metrics. In the DT method, the accuracy reached 92% with a sensitivity of 91%. RF showed improved performance with an accuracy and sensitivity of 95.77% each. ELM produced an accuracy of 93.42% with a computation time duration of 0.18 s. CatBoost achieved better results, with an accuracy and sensitivity of 99%. Meanwhile, the combination of XGBoost with IForest as the outlier detection method used in this study produced the highest performance with 100% accuracy, sensitivity, and specificity, respectively, and a computation time of 0.36s.

There are several recommendations for future research, including that the outlier detection method used in this research is based on unsupervised learning, so future research is recommended to use supervised learning methods such as Fuzzy Min-Max Neural Network (FMN), where the class pattern is defined as a combination of fuzzy sets [51]. This research conducted various tests on XGBoost parameters such as learning rate (η), max depth, and estimator. In future research, optimization methods such as Genetic Algorithm (GA) or Particle Swarm Optimization (PSO) can be applied to further optimize the parameters in classification, thus improving the efficiency and overall performance of the model [52].

4. CONCLUSIONS

Based on the results of fetal health status classification using XGBoost and outlier detection with IForest, it can be concluded that IForest effectively detects outliers without changing the central tendency of the data, as evidenced by similar mean values and lower standard deviations in the inlier data. The maximum value decreases, indicating the removal of extreme values, while the minimum value and mode remain consistent. From 2126 data, IForest reduced the data to 1956 after removing the outliers, speeding up the computation with 100% accuracy, sensitivity, and specificity which is an improvement of 3.76%, 9.41%, and 4.75% from the scheme without outlier handling. The optimal parameters are η=0.01, max depth=7, and estimator=100 with a computation time of 0.36 s which is 0.51 s more efficient than without outlier handling. This result shows that IForest improves computational efficiency without degrading classification performance. In addition, speed in the diagnosis process can also help medical personnel to provide faster action, so that potential delays in patient treatment can be reduced.

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